

Supplemental Table 3

overlap with HIF2A targets			
Gene Symbol	Fold Change	P-Value	Full name
STC2	4.26	2.76E-22	stanniocalcin 2
DDIT4	3.76	4.33E-20	DNA-damage-inducible transcript 4
PNMA2	2.63	3.14E-10	paraneoplastic antigen MA2
STC1	2.4	0	stanniocalcin 1
VEGFA	2.17	7.87E-10	vascular endothelial growth factor A
ANKRD37	2.07	0.00000048	ankyrin repeat domain 37
DDIT3	2.06	7.36E-08	DNA-damage-inducible transcript 3
TMEM158	1.95	0.000000048	transmembrane protein 158 (gene/pseudogene)
C1orf51	1.82	0.000901	chromosome 1 open reading frame 51
BNIP3L	1.76	1.01E-19	BCL2/adenovirus E1B 19kDa interacting protein 3-like
SAP30	1.74	0.000000518	Sin3A-associated protein, 30kDa
GPR176	1.74	1.16E-21	G protein-coupled receptor 176
GCNT2	1.73	3.91E-14	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
ARTN	1.7	0.000825	artemin
LRIG1	1.63	0.0000433	leucine-rich repeats and immunoglobulin-like domains 1
LRP8	1.62	0.0000625	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
			solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
SLC1A1	1.62	0.000139	solute carrier family 2 (facilitated glucose transporter), member 1
SLC2A1	1.59	0.0000408	
ENO2	1.55	0.000122	enolase 2 (gamma, neuronal)
	1.54	0.000945	
B3GNT4	1.49	0.01	UDP-GlcNAc:betaGal beta-1,3-N-acetylglicosaminyltransferase 4
			family with sequence similarity 101, member B
FAM101B	1.47	0.00201	
	1.46	0.00209	mixed lineage kinase 4
CXCR4	1.46	0.000914	chemokine (C-X-C motif) receptor 4
ZNF395	1.46	0.000952	zinc finger protein 395
GPR98	1.45	0.00193	G protein-coupled receptor 98
MRPS21	1.4	0.00274	mitochondrial ribosomal protein S21
NKD2	1.4	0.01	naked cuticle homolog 2 (<i>Drosophila</i>)
ADM	1.39	0.00353	adrenomedullin
RNASET2	1.38	0.00875	ribonuclease T2
PDLIM2	1.38	0.00503	PDZ and LIM domain 2 (mystique)
			protein phosphatase 1, regulatory (inhibitor)
PPP1R3B	1.37	0.00565	subunit 3B
	1.34	0.01	major facilitator superfamily domain containing 10
RBPJ	1.33	1.03E-08	recombination signal binding protein for immunoglobulin kappa J region
TSPAN2	1.28	0.000357	tetraspanin 2
TNFAIP6	1.25	0.00565	tumor necrosis factor, alpha-induced protein 6
JUN	1.21	0.00204	jun proto-oncogene

KLF7	1.19	0.00324	Kruppel-like factor 7 (ubiquitous)
Gene Symbol	Gene Ontology		
STC2	response to vitamin D [GO:0033280]; response to peptide hormone stimulus [GO:0043434]; cellular response to hypoxia [GO:0071456]; cell surface receptor linked signaling pathway [GO:0007166]; response to nutrient [GO:0007584]; decidualization [GO:0046697]; cell-cell signaling [GO:0007267]; embryo implantation [GO:0007566]		
DDIT4	negative regulation of TOR signaling cascade [GO:0032007]; protein complex disassembly [GO:0043241]; negative regulation of glycolysis [GO:0045820]; apoptosis [GO:0006915]; response to hypoxia [GO:0001666]; reactive oxygen species metabolic process [GO:0072593]		
PNMA2	apoptosis [GO:0006915]		
STC1	cellular calcium ion homeostasis [GO:0006874]; activation of JUN kinase activity [GO:0007257]; cellular response to glucocorticoid stimulus [GO:0071385]; regulation of translation [GO:0006417]; phosphate transport [GO:0006817]; induction of apoptosis [GO:0006917]; regulation of superoxide anion generation [GO:0032928]; regulation of cellular respiration [GO:0043457]; regulation of steroid biosynthetic process [GO:0050810]; mitochondrial calcium ion transport [GO:0006851]; response to vitamin D [GO:0033280]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; cellular response to cAMP [GO:0071320]; skeletal system development [GO:0001501]; osteoblast development [GO:0002076]; muscle organ development [GO:0007517]; response to organic cyclic compound [GO:0014070]; cartilage development [GO:0051216]; granulosa cell differentiation [GO:0060014]; cellular response to hypoxia [GO:0071456]; angiogenesis [GO:0001525]; response to oxidative stress [GO:0006979]; cell surface receptor linked signaling pathway [GO:0007166]; response to nutrient [GO:0007584]; electron transport chain [GO:0022900]; regulation of ossification [GO:0030278]; decidualization [GO:0046697]; ossification [GO:0001503]; cell-cell signaling [GO:0007267]; embryo implantation [GO:0007566]; regulation of cell proliferation [GO:0042127]; reproduction [GO:0000003]; growth [GO:0040007]		

peptidyl-tyrosine phosphorylation [GO:0050927]; positive regulation of blood vessel endothelial cell migration [GO:0060754]; positive regulation of transcription from RNA polymerase II promoter [GO:0090190]; mRNA stabilization [GO:0001570]; cardiac muscle fiber development [GO:0001822]; anti-apoptosis [GO:0001938]; positive regulation of endothelial cell migration [GO:0002575]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0002576]; endothelial cell chemotaxis [GO:0003007]; eye photoreceptor cell development [GO:0007399]; positive regulation of vascular permeability [GO:0007498]; platelet-derived growth factor receptor signaling pathway [GO:0030335]; vascular endothelial growth factor receptor signaling pathway [GO:0030855]; induction of positive chemotaxis [GO:0045766]; primitive erythrocyte differentiation [GO:0048661]; in utero embryonic development [GO:0048844]; T-helper 1 type immune response [GO:0033138]; negative regulation of apoptosis [GO:0050731]; surfactant homeostasis [GO:0043536]; positive regulation of MAP kinase activity [GO:0045944]; negative regulation of bone resorption [GO:0048255]; camera-type eye morphogenesis [GO:0048739]; positive regulation of positive chemotaxis [GO:0006916]; positive regulation of mast cell chemotaxis [GO:0010595]; positive regulation of branching involved in ureteric bud morphogenesis [GO:0030949]; vasculogenesis [GO:0035767]; kidney development [GO:0042462]; positive regulation of endothelial cell proliferation [GO:0043117]; basophil chemotaxis [GO:0048008]; platelet degranulation [GO:0048010]; heart morphogenesis [GO:0050930]; nervous system development [GO:0060319]; mesoderm development [GO:0001701]; positive regulation of cell migration [GO:0042088]; epithelial cell differentiation [GO:0043066]; positive regulation of angiogenesis [GO:0043129]; positive regulation of smooth muscle cell proliferation [GO:0043406]; artery morphogenesis [GO:0045779]; positive chemotaxis [GO:0050918]; cellular response to hypoxia [GO:0071456]; angiogenesis [GO:0001525]; ovarian follicle development [GO:0001541]; patterning of blood vessels [GO:0001569]; response to hypoxia [GO:0001666]; blood vessel remodeling [GO:0001974]; positive regulation of mesenchymal cell proliferation [GO:0002053]; positive regulation of leukocyte migration [GO:0002687]; lactation [GO:0007595]; blood coagulation [GO:0007596]; regulation of cell shape [GO:0008360]; response to cold [GO:0009409]; platelet activation [GO:0030168]; post-embryonic camera-type eye development [GO:0031077]; positive regulation of cell adhesion [GO:0045785]; lung alveolus development [GO:0048286]; cell maturation [GO:0048469]; positive regulation

ANKRD37

negative regulation of canonical Wnt receptor signaling pathway [GO:0090090]; regulation of transcription, DNA-dependent [GO:0006355]; mRNA transcription from RNA polymerase II promoter [GO:0042789]; positive regulation of transcription, DNA-dependent [GO:0045893]; response to amphetamine [GO:0001975]; negative regulation of CREB transcription factor activity [GO:0032792]; response to hydrogen peroxide [GO:0042542]; positive regulation of apoptosis [GO:0043065]; negative regulation of determination of dorsal identity [GO:2000016]; transcription, DNA-dependent [GO:0006351]; response to DNA damage stimulus [GO:0006974]; ER overload response [GO:0006983]; endoplasmic reticulum unfolded protein response [GO:0030968]; response to endoplasmic reticulum stress [GO:0034976]; negative regulation of sequence-specific DNA binding transcription factor activity [GO:0043433]; regulation of DNA-dependent transcription in response to stress [GO:0043620]; response to oxidative stress [GO:0006979]; cell cycle arrest [GO:0007050]; response to nutrient [GO:0007584]; response to drug [GO:0042493]; cell redox homeostasis [GO:0045454]; embryonic organ development [GO:0048568]; cell cycle [GO:0007049]; aging [GO:0007568]

TMEM158	
	regulation of cell cycle [GO:0051726]; aging [GO:0007568]; response to chemical stimulus [GO:0042221]
C1orf51	
BNIP3L	induction of apoptosis [GO:0006917]; mitochondrial protein catabolic process [GO:0035694]; negative regulation of survival gene product expression [GO:0008634]; positive regulation of apoptosis [GO:0043065]; negative regulation of apoptosis [GO:0043066]; defense response to virus [GO:0051607]; negative regulation of cell proliferation [GO:0008285]; interspecies interaction between organisms [GO:0044419]; cellular process [GO:0009987]
SAP30	chromatin remodeling [GO:0006338]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; histone deacetylation [GO:0016575]; regulation of transcription, DNA-dependent [GO:0006355]; protein import into nucleus, translocation [GO:0000060]; positive regulation of protein binding [GO:0032092]; positive regulation of DNA binding [GO:0043388]
GPR176	G-protein coupled receptor protein signaling pathway [GO:0007186]; synaptic transmission [GO:0007268]
GCNT2	glycosaminoglycan biosynthetic process [GO:0006024]; visual perception [GO:0007601]; protein O-linked glycosylation [GO:0006493]; multicellular organismal development [GO:0007275]
ARTN	positive regulation of neuron projection development [GO:0010976]; transmembrane receptor protein tyrosine kinase signaling pathway [GO:0007169]; axon guidance [GO:0007411]; central nervous system development [GO:0007417]; neuroblast proliferation [GO:0007405]; signal transduction [GO:0007165]; positive regulation of cell proliferation [GO:0008284]
LRIG1	

LRP8	proteolysis [GO:0006508]; cytokine-mediated signaling pathway [GO:0019221]; lipid metabolic process [GO:0006629]; endocytosis [GO:0006897]; blood coagulation [GO:0007596]; hippocampus development [GO:0021766]; layer formation in cerebral cortex [GO:0021819]; platelet activation [GO:0030168]; signal transduction [GO:0007165]
SLC1A1	protein homooligomerization [GO:0051260]; L-glutamate import [GO:0051938]; D-aspartate import [GO:0070779]; dicarboxylic acid transport [GO:0006835]; L-glutamate transport [GO:0015813]; ion transport [GO:0006811]; synaptic transmission [GO:0007268]; transmembrane transport [GO:0055085]
SLC2A1	glucose transport [GO:0015758]; hexose transport [GO:0008645]; regulation of insulin secretion [GO:0050796]; energy reserve metabolic process [GO:0006112]; water-soluble vitamin metabolic process [GO:0006767]; carbohydrate transport [GO:0008643]; carbohydrate metabolic process [GO:0005975]; vitamin metabolic process [GO:0006766]; response to osmotic stress [GO:0006970]; transmembrane transport [GO:0055085]
ENO2	glucose metabolic process [GO:0006006]; gluconeogenesis [GO:0006094]; response to estradiol stimulus [GO:0032355]; glycolysis [GO:0006096]; response to organic cyclic compound [GO:0014070]; carbohydrate metabolic process [GO:0005975]; response to drug [GO:0042493]
B3GNT4	poly-N-acetyllactosamine biosynthetic process [GO:0030311]; protein glycosylation [GO:0006486]
FAM101B	activation of JUN kinase activity [GO:0007257]; peptidyl-tyrosine phosphorylation [GO:0018108]; protein autophosphorylation [GO:0046777]; protein phosphorylation [GO:0006468]

	<p>cytosolic calcium ion concentration [GO:0007204]; activation of JAK2 kinase activity [GO:0042977]; positive regulation of peptidyl-serine phosphorylation of STAT protein [GO:0033141]; positive regulation of Rho protein signal transduction [GO:0035025]; positive regulation of actin filament polymerization [GO:0030838]; positive regulation of interleukin-6 biosynthetic process [GO:0045410]; positive regulation of interleukin-8 biosynthetic process [GO:0045416]; protein homooligomerization [GO:0051260]; response to dexamethasone stimulus [GO:0071548]; activation of MAPK activity [GO:0000187]; anti-apoptosis [GO:0006916]; induction of apoptosis [GO:0006917]; regulation of T cell chemotaxis [GO:0010819]; Rac protein signal transduction [GO:0016601]; actin filament polymerization [GO:0030041]; regulation of estrogen receptor signaling pathway [GO:0033146]; negative regulation of phosphorylation [GO:0042326]; positive regulation of phosphorylation [GO:0042327]; positive regulation of DNA replication [GO:0045740]; negative regulation of G-protein coupled receptor protein signaling pathway [GO:0045744]; positive regulation of oligodendrocyte differentiation [GO:0048714]; activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway [GO:0007205]; JAK-STAT cascade [GO:0007259]; regulation of G-protein coupled receptor protein signaling pathway [GO:0008277]; calcium-mediated signaling [GO:0019722]; cell projection assembly [GO:0030031]; entry into host cell [GO:0030260]; response to prostaglandin E stimulus [GO:0034695]; response to interferon-alpha [GO:0035455]; response to cocaine [GO:0042220]; regulation of apoptosis [GO:0042981]; negative regulation of apoptosis [GO:0043066]; positive regulation of epidermal growth factor receptor activity [GO:0045741]; regulation of calcium-mediated signaling [GO:0050848]; response to prostaglandin D stimulus [GO:0071798]; dendritic cell chemotaxis [GO:0002407]; positive regulation of leukocyte chemotaxis [GO:0002690]; receptor-mediated endocytosis [GO:0006898]; apoptosis [GO:0006915]; induction by virus of host cell-cell fusion [GO:0006948]; inflammatory response [GO:0006954]; G-protein coupled receptor protein signaling pathway [GO:0007186]; integrin-mediated signaling pathway [GO:0007229]; intracellular protein kinase cascade [GO:0007243]; detection of virus [GO:0009597]; positive regulation of cell-cell adhesion [GO:0022409]; regulation of endocytosis [GO:0030100]; regulation of cell migration [GO:0030334]; positive regulation of cell migration [GO:0030335]; negative regulation of cell migration [GO:0030336]; neutrophil chemotaxis [GO:0030593]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-2</p>
CXCR4	
ZNF395	<p>regulation of transcription, DNA-dependent [GO:0006355]; response to oxidative stress [GO:0006979]</p>
GPR98	<p>sensory perception of sound [GO:0007605]; neuropeptide signaling pathway [GO:0007218]; sensory perception of light stimulus [GO:0050953]; inner ear receptor stereocilium organization [GO:0060122]; detection of calcium ion [GO:0005513]; G-protein coupled receptor protein signaling pathway [GO:0007186]; nervous system development [GO:0007399]; photoreceptor cell maintenance [GO:0045494]; maintenance of organ identity [GO:0048496]; detection of mechanical stimulus involved in sensory perception of sound [GO:0050910]; cell-cell adhesion [GO:0016337]; inner ear development [GO:0048839]; neurological system process [GO:0050877]; cell communication [GO:0007154]; response to stimulus [GO:0050896]</p>
MRPS21	<p>translation [GO:0006412]</p>

NKD2

negative regulation of canonical Wnt receptor signaling pathway [GO:0090090]; protein targeting to membrane [GO:0006612]; negative regulation of Wnt receptor signaling pathway [GO:0030178]; Wnt receptor signaling pathway [GO:0016055]; cell fate determination [GO:0001709]; exocytosis [GO:0006887]; transport [GO:0006810]

ADM

elevation of cytosolic calcium ion concentration [GO:0007204]; calcium ion homeostasis [GO:0055074]; cAMP biosynthetic process [GO:0006171]; cAMP-mediated signaling [GO:0019933]; response to glucocorticoid stimulus [GO:0051384]; neural tube closure [GO:0001843]; progesterone biosynthetic process [GO:0006701]; androgen metabolic process [GO:0008209]; response to insulin stimulus [GO:0032868]; odontogenesis of dentine-containing tooth [GO:0042475]; negative regulation of vasoconstriction [GO:0045906]; positive regulation of vasodilation [GO:0045909]; heart development [GO:0007507]; blood circulation [GO:0008015]; positive regulation of heart rate [GO:0010460]; organ regeneration [GO:0031100]; neuron projection regeneration [GO:0031102]; response to lipopolysaccharide [GO:0032496]; positive regulation of anti-apoptosis [GO:0045768]; branching involved in embryonic placenta morphogenesis [GO:0060670]; response to hypoxia [GO:0001666]; regulation of the force of heart contraction [GO:0002026]; response to cold [GO:0009409]; response to wounding [GO:0009611]; response to organic substance [GO:0010033]; response to starvation [GO:0042594]; hormone secretion [GO:0046879]; spongiotrophoblast layer development [GO:0060712]; signal transduction [GO:0007165]; cell-cell signaling [GO:0007267]; female pregnancy [GO:0007565]; aging [GO:0007568]; positive regulation of cell proliferation [GO:0008284]; negative regulation of cell proliferation [GO:0008285]; developmental growth [GO:0048589]

RNASET2

RNA catabolic process [GO:0006401]; negative regulation of cell growth [GO:0030308]; aging [GO:0007568]; negative regulation of cell proliferation [GO:0008285]

PDLIM2	insulin-like growth factor receptor signaling pathway [GO:0048009]; negative regulation of NF-kappaB transcription factor activity [GO:0032088]; regulation of tumor necrosis factor production [GO:0032680]; positive regulation of cell migration [GO:0030335]; response to lipopolysaccharide [GO:0032496]; positive regulation of cell adhesion [GO:0045785]; signal transduction [GO:0007165]; negative regulation of cell proliferation [GO:0008285]; response to chemical stimulus [GO:0042221]
PPP1R3B	glucan biosynthetic process [GO:0009250]; positive regulation of glycogen biosynthetic process [GO:0045725]; glycogen metabolic process [GO:0005977]; DNA replication [GO:0006260]; protein dephosphorylation [GO:0006470]; enzyme linked receptor protein signaling pathway [GO:0007167]; carbohydrate transport [GO:0008643]; carbohydrate metabolic process [GO:0005975]; cell differentiation [GO:0030154]; regulation of cell cycle [GO:0051726]; multicellular organismal development [GO:0007275]; cellular metabolic process [GO:0044237]; primary metabolic process [GO:0044238]; metabolic process [GO:0008152]; regulation of biological process [GO:0050789]
RBPJ	organic anion transport [GO:0015711]; tetracycline transport [GO:0015904]; apoptosis [GO:0006915]; drug transport [GO:0015893]; response to drug [GO:0042493]; transport [GO:0006810]; transmembrane transport [GO:0055085]
TSPAN2	regulation of transcription, DNA-dependent [GO:0006355]; positive regulation of transcription of Notch receptor target [GO:0007221]; negative regulation of transcription, DNA-dependent [GO:0045892]; DNA recombination [GO:0006310]; transcription, DNA-dependent [GO:0006351]; gene expression [GO:0010467]
TNFAIP6	brain development [GO:0007420]; cellular component movement [GO:0006928]; cell adhesion [GO:0007155]; cell proliferation [GO:0008283]
	positive regulation of prostaglandin biosynthetic process [GO:0031394]; negative regulation of BMP signaling pathway [GO:0030514]; SMAD protein import into nucleus [GO:0007184]; negative regulation of phosphorylation [GO:0042326]; regulation of osteoclast differentiation [GO:0045670]; extracellular matrix organization [GO:0030198]; negative regulation of osteoblast differentiation [GO:0045668]; inflammatory response [GO:0006954]; regulation of bone remodeling [GO:0046850]; cell adhesion [GO:0007155]; signal transduction [GO:0007165]; cell-cell signaling [GO:0007267]

negative regulation of protein autophosphorylation [GO:0031953]; positive regulation of Rho GTPase activity [GO:0032321]; MyD88-dependent toll-like receptor signaling pathway [GO:0002755]; MyD88-independent toll-like receptor signaling pathway [GO:0002756]; toll-like receptor 1 signaling pathway [GO:0034130]; toll-like receptor 2 signaling pathway [GO:0034134]; toll-like receptor 3 signaling pathway [GO:0034138]; toll-like receptor 4 signaling pathway [GO:0034142]; positive regulation of monocyte differentiation [GO:0045657]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; microglial cell activation [GO:0001774]; release of cytochrome c from mitochondria [GO:0001836]; toll-like receptor signaling pathway [GO:0002224]; transforming growth factor beta receptor signaling pathway [GO:0007179]; SMAD protein import into nucleus [GO:0007184]; learning [GO:0007612]; positive regulation by host of viral transcription [GO:0043923]; positive regulation of DNA replication [GO:0045740]; negative regulation of transcription, DNA-dependent [GO:0045892]; positive regulation of transcription, DNA-dependent [GO:0045893]; stress-activated MAPK cascade [GO:0051403]; membrane depolarization [GO:0051899]; cellular response to calcium ion [GO:0071277]; axon regeneration [GO:0031103]; leading edge cell differentiation [GO:0035026]; response to hydrogen peroxide [GO:0042542]; negative regulation of DNA binding [GO:0043392]; negative regulation of neuron apoptosis [GO:0043524]; positive regulation of neuron apoptosis [GO:0043525]; cellular response to potassium ion starvation [GO:0051365]; liver development [GO:0001889]; positive regulation of endothelial cell proliferation [GO:0001938]; transcription, DNA-dependent [GO:0006351]; Toll signaling pathway [GO:0008063]; response to organic cyclic compound [GO:0014070]; response to lipopolysaccharide [GO:0032496]; response to cytokine stimulus [GO:0034097]; negative regulation by host of viral transcription [GO:0043922]; positive regulation of smooth muscle cell proliferation [GO:0048661]; response to cAMP [GO:0051591]; SMAD protein signal transduction [GO:0060395]; angiogenesis [GO:0001525]; outflow tract morphogenesis [GO:0003151]; response to radiation [GO:0009314]; response to mechanical stimulus [GO:0009612]; response to drug [GO:0042493]; innate immune response [GO:0045087]; positive regulation of fibroblast proliferation [GO:0048146]; regulation of sequence-specific DNA binding transcription factor activity [GO:0051090]; regulation of cell cycle [GO:0051726]; aging [GO:0007568]; circadian rhythm [GO:0007623]; negative regulation of cell proliferation [GO:0008285]; cellular process [GO:0009987]

KLF7
 negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; regulation of transcription from RNA polymerase II promoter [GO:0006357]; negative regulation of insulin secretion [GO:0046676]; response to morphine [GO:0043278]; positive regulation of transcription, DNA-dependent [GO:0045893]; regulation of cytokine secretion [GO:0050707]; negative regulation of fat cell differentiation [GO:0045599]; transcription, DNA-dependent [GO:0006351]; nervous system development [GO:0007399]; axon guidance [GO:0007411]; dendrite morphogenesis [GO:0048813]; response to drug [GO:0042493]

overlap with HIF1A targets

Gene Symbol	Fold Change	P-Value	Full name
SLC16A3	7.15	7.8E-29	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)
BNIP3	5.26	3.29E-25	BCL2/adenovirus E1B 19kDa interacting protein 3
DDIT4	4.21	1.35E-19	
	3.76	4.33E-20	DNA-damage-inducible transcript 4

PGK1	3.65	2.03E-23	phosphoglycerate kinase 1
TXNIP	3.23	1.96E-17	thioredoxin interacting protein
EGLN1	3.2	1.5E-25	egl nine homolog 1 (C. elegans)
PDK1	3.15	6.86E-14	pyruvate dehydrogenase kinase, isozyme 1
ALDOC	2.79	5.53E-15	aldolase C, fructose-bisphosphate ribosomal modification protein rimK-like
FAM80A	2.71	0.0000171	family member A
TMEM45A	2.62	1.19E-13	transmembrane protein 45A
RORA	2.52	4.63E-09	RAR-related orphan receptor A
PGM1	2.48	2.27E-13	phosphoglucomutase 1
	2.39	0.00141	chromosome 4 open reading frame 47
SPAG4	2.27	0.000000734	sperm associated antigen 4
	2.24	3.28E-11	chromosome 4 open reading frame 3
HK2	2.2	7.9E-11	hexokinase 2
ZNF160	2.18	2.95E-11	zinc finger protein 160
VEGFA	2.17	7.87E-10	vascular endothelial growth factor A
WDR54	2.1	8.47E-10	WD repeat domain 54
SLC2A14	2.1	4.85E-09	solute carrier family 2 (facilitated glucose transporter), member 14
ANKRD37	2.07	0.00000048	ankyrin repeat domain 37
DDIT3	2.06	7.36E-08	DNA-damage-inducible transcript 3
PFKFB4	2.01	2.93E-08	6-phosphofructo-2-kinase/fructose-2,6- biphosphatase 4
ISG20	2	0.00103	interferon stimulated exonuclease gene 20kDa
VLDLR	1.94	0.000000155	very low density lipoprotein receptor
MT1X	1.92	2.62E-08	metallothionein 1X
GPR160	1.91	0.00000204	G protein-coupled receptor 160
P4HA1	1.83	0.000000132	prolyl 4-hydroxylase, alpha polypeptide I
JMJD1A	1.82	0.000000599	lysine (K)-specific demethylase 3A
JMJD2C	1.82	0.000746	lysine (K)-specific demethylase 4C
KIAA1244	1.77	0.00702	KIAA1244
TNNT1	1.77	0.00000432	troponin T type 1 (skeletal, slow)
BNIP3L	1.76	1.01E-19	BCL2/adenovirus E1B 19kDa interacting protein 3-like
CDA	1.75	0.0000634	cytidine deaminase
SAP30	1.74	0.000000518	Sin3A-associated protein, 30kDa
GPI	1.72	5.46E-20	glucose-6-phosphate isomerase
GBE1	1.68	1.68E-10	glucan (1,4-alpha-), branching enzyme 1
	1.66	0.01	
WSB1	1.65	0.00000395	WD repeat and SOCS box-containing 1
SLC1A1	1.62	0.000139	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
P4HA2	1.61	0.0000324	prolyl 4-hydroxylase, alpha polypeptide II
SLC2A1	1.59	0.0000408	solute carrier family 2 (facilitated glucose transporter), member 1
ENO2	1.55	0.000122	enolase 2 (gamma, neuronal)
B3GNT4	1.49	0.01	UDP-GlcNAc:betaGal beta-1,3-N- acetylglucosaminyltransferase 4
ANKZF1	1.46	0.00232	ankyrin repeat and zinc finger domain containing 1
CXCR4	1.46	0.000914	chemokine (C-X-C motif) receptor 4
ZNF395	1.46	0.000952	zinc finger protein 395

ADM	1.39	0.00353	adrenomedullin
PDLIM2	1.38	0.00503	PDZ and LIM domain 2 (mystique) protein phosphatase 1, regulatory (inhibitor) subunit 3B
PPP1R3B	1.37	0.00565	eukaryotic translation initiation factor 4A2
EIF4A2	1.35	0.00575	peptidylglycine alpha-amidating monooxygenase
PAM	1.32	0.00223	ERO1-like (<i>S. cerevisiae</i>)
ERO1L	1.32	0.01	
PDK3	1.31	0.0000199	pyruvate dehydrogenase kinase, isozyme 3
PLOD2	1.24	0.00348	procollagen-lysine, 2-oxoglutarate 5- dioxygenase 2
JUN	1.21	0.00204	jun proto-oncogene
KLF7	1.19	0.00324	Kruppel-like factor 7 (ubiquitous)

Gene Symbol	Gene Ontology
SLC16A3	pyruvate metabolic process [GO:0006090]; monocarboxylic acid transport [GO:0015718]; lactate transport [GO:0015727]; organic anion transport [GO:0015711]; intracellular protein transport [GO:0006886]; response to hypoxia [GO:0001666]; blood coagulation [GO:0007596]; leukocyte migration [GO:0050900]; transmembrane transport [GO:0055085]
BNIP3	chromatin remodeling [GO:0006338]; induction of apoptosis by intracellular signals [GO:0008629]; positive regulation of release of cytochrome c from mitochondria [GO:0090200]; DNA fragmentation involved in apoptotic nuclear change [GO:0006309]; anti-apoptosis [GO:0006916]; induction of apoptosis [GO:0006917]; mitochondrial fragmentation involved in apoptosis [GO:0043653]; negative regulation of membrane potential [GO:0045837]; cellular response to hydrogen peroxide [GO:0070301]; cellular response to cobalt ion [GO:0071279]; negative regulation of survival gene product expression [GO:0008634]; negative regulation of mitochondrial fusion [GO:0010637]; positive regulation of protein complex disassembly [GO:0043243]; brown fat cell differentiation [GO:0050873]; positive regulation of mitochondrial fission [GO:0090141]; apoptosis [GO:0006915]; autophagic cell death [GO:0048102]; neuron apoptosis [GO:0051402]; cellular response to mechanical stimulus [GO:0071260]; cellular response to hypoxia [GO:0071456]; response to hypoxia [GO:0001666]; regulation of mitochondrial membrane permeability [GO:0046902]; defense response to virus [GO:0051607]; response to hyperoxia [GO:0055093]; reactive oxygen species metabolic process [GO:0072593]; cell death [GO:0008219]; interspecies interaction between organisms [GO:0044419]
DDIT4	negative regulation of TOR signaling cascade [GO:0032007]; protein complex disassembly [GO:0043241]; negative regulation of glycolysis [GO:0045820]; apoptosis [GO:0006915]; response to hypoxia [GO:0001666]; reactive oxygen species metabolic process [GO:0072593]
PGK1	glucose metabolic process [GO:0006006]; gluconeogenesis [GO:0006094]; phosphorylation [GO:0016310]; glycolysis [GO:0006096]; carbohydrate metabolic process [GO:0005975]

	regulation of histone H3-K9 methylation [GO:0051570]; response to glucose stimulus [GO:0009749]; regulation of glucose metabolic process [GO:0010906]; chromatin modification [GO:0016568]; regulation of histone acetylation [GO:0035065]; negative regulation of glucose import [GO:0046325]; regulation of transcription, DNA-dependent [GO:0006355]; protein import into nucleus [GO:0006606]; macrophage differentiation [GO:0030225]; response to estradiol stimulus [GO:0032355]; platelet-derived growth factor receptor signaling pathway [GO:0048008]; keratinocyte differentiation [GO:0030216];
TXNIP	response to progesterone stimulus [GO:0032570]; response to hydrogen peroxide [GO:0042542]; positive regulation of apoptosis [GO:0043065]; regulation of epidermis development [GO:0045682]; regulation of inflammatory response [GO:0050727]; response to calcium ion [GO:0051592]; epithelial cell differentiation [GO:0030855]; cellular response to tumor cell [GO:0071228]; activation of innate immune response [GO:0002218]; response to oxidative stress [GO:0006979]; cell cycle arrest [GO:0007050]; response to mechanical stimulus [GO:0009612]; response to drug [GO:0042493]; innate immune response [GO:0045087]; negative regulation of cell division [GO:0051782]; response to stress [GO:0006950]; immune response [GO:0006955]; cell cycle [GO:0007049]; aging [GO:0007568]; biosynthetic process [GO:0009058]; regulation of cell proliferation [GO:0042127]
EGLN1	oxygen homeostasis [GO:0032364]; negative regulation of sequence-specific DNA binding transcription factor activity [GO:0043433]; response to hypoxia [GO:0001666]
PDK1	glucose metabolic process [GO:0006006]; pyruvate metabolic process [GO:0006090]; positive regulation of epithelial cell migration [GO:0010634]; peptidyl-serine phosphorylation [GO:0018105]; peptidyl-histidine phosphorylation [GO:0018106]; negative regulation of transforming growth factor beta receptor signaling pathway [GO:0030512]; positive regulation of I-kappaB kinase/NF-kappaB cascade [GO:0043123]; positive regulation of MAPKKK cascade [GO:0043410]; regulation of JNK cascade [GO:0046328]; positive regulation of protein kinase B signaling cascade [GO:0051897]; anti-apoptosis [GO:0006916]; induction of apoptosis [GO:0006917]; SMAD protein import into nucleus [GO:0007184]; insulin receptor signaling pathway [GO:0008286]; regulation of acetyl-CoA biosynthetic process from pyruvate [GO:0010510]; negative regulation of kinase activity [GO:0033673]; regulation of phosphorylation [GO:0042325]; regulation of protein kinase B signaling cascade [GO:0051896]; regulation of protein kinase C signaling cascade [GO:0090036]; protein phosphorylation [GO:0006468]; regulation of phosphatidylinositol 3-kinase cascade [GO:0014066]; response to insulin stimulus [GO:0032868]; regulation of membrane potential [GO:0042391]; negative regulation of apoptosis [GO:0043066]; positive regulation of NF-kappaB transcription factor activity [GO:0051092]; regulation of focal adhesion assembly [GO:0051893]; protein complex assembly [GO:0006461]; small GTPase mediated signal transduction [GO:0007264]; regulation of protein localization [GO:0032880]; regulation of cell growth [GO:0001558]; carbohydrate metabolic process [GO:0005975]; cell cycle arrest [GO:0007050]; cell surface receptor linked signaling pathway [GO:0007166]; actin cytoskeleton organization [GO:0030036]; regulation of sequence-specific DNA binding transcription factor activity [GO:0051090]; regulation of binding [GO:0051098]; regulation of cell cycle [GO:0051726]; regulation of cell proliferation [GO:0042127]

	protein homotetramerization [GO:0051289]; protein heterotetramerization [GO:0051290]; fructose metabolic process [GO:0006000]; glucose metabolic process [GO:0006006]; gluconeogenesis [GO:0006094]; fructose 1,6-bisphosphate metabolic process [GO:0030388]; glycolysis [GO:0006096]; apoptosis [GO:0006915]; response to organic cyclic compound [GO:0014070]; organ regeneration [GO:0031100]; response to hypoxia [GO:0001666]; carbohydrate metabolic process [GO:0005975]; response to organic nitrogen [GO:0010243]; aging [GO:0007568]
FAM80A	protein modification process [GO:0006464]; glutathione biosynthetic process [GO:0006750]; peptide metabolic process [GO:0006518]
TMEM45A	response to hypoxia [GO:0001666]
RORA	regulation of transcription from RNA polymerase II promoter by nuclear hormone receptor [GO:0034339]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; cGMP metabolic process [GO:0046068]; regulation of macrophage activation [GO:0043030]; transcription, DNA-dependent [GO:0006351]; nitric oxide biosynthetic process [GO:0006809]; cerebellar Purkinje cell differentiation [GO:0021702]; gene expression [GO:0010467]; intracellular receptor mediated signaling pathway [GO:0030522]; signal transduction [GO:0007165]
PGM1	glycogen biosynthetic process [GO:0005978]; glycogen catabolic process [GO:0005980]; trehalose biosynthetic process [GO:0005992]; glucose metabolic process [GO:0006006]; glucose 1-phosphate metabolic process [GO:0019255]; galactose catabolic process [GO:0019388]; carbohydrate metabolic process [GO:0005975]
SPAG4	spermatogenesis [GO:0007283]; multicellular organismal process [GO:0032501]
HK2	glucose metabolic process [GO:0006006]; glucose transport [GO:0015758]; hexose
ZNF160	negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; regulation of transcription, DNA-dependent [GO:0006355]; hemopoiesis [GO:0030097]; response to lipopolysaccharide [GO:0032496]; multicellular organismal development [GO:0007275]; cellular homeostasis [GO:0019725]; establishment of protein localization [GO:0045184]

	positive regulation of peptidyl-serine phosphorylation [GO:0040000]; positive regulation of peptidyl-tyrosine phosphorylation [GO:0050927]; positive regulation of blood vessel endothelial cell migration [GO:0060754]; positive regulation of transcription from RNA polymerase II promoter [GO:0090190]; mRNA stabilization [GO:0001570]; cardiac muscle fiber development [GO:0001822]; anti-apoptosis [GO:0001938]; positive regulation of endothelial cell migration [GO:0002575]; positive regulation of vascular endothelial growth factor receptor signaling pathway [GO:0002576]; endothelial cell chemotaxis [GO:0003007]; eye photoreceptor cell development [GO:0007399]; positive regulation of vascular permeability [GO:0007498]; platelet-derived growth factor receptor signaling pathway [GO:0030335]; vascular endothelial growth factor receptor signaling pathway [GO:0030855]; induction of positive chemotaxis [GO:0045766]; primitive erythrocyte differentiation [GO:0048661]; in utero embryonic development [GO:0048844]; T-helper 1 type immune response [GO:0033138]; negative regulation of apoptosis [GO:0050731]; surfactant homeostasis [GO:0043536]; positive regulation of MAP kinase activity [GO:0045944]; negative regulation of bone resorption [GO:0048255]; camera-type eye morphogenesis [GO:0048739]; positive regulation of positive chemotaxis [GO:0006916]; positive regulation of mast cell chemotaxis [GO:0010595]; positive regulation of branching involved in ureteric bud morphogenesis [GO:0030949]; vasculogenesis [GO:0035767]; kidney development [GO:0042462]; positive regulation of endothelial cell proliferation [GO:0043117]; basophil chemotaxis [GO:0048008]; platelet degranulation [GO:0048010]; heart morphogenesis [GO:0050930]; nervous system development [GO:0060319]; mesoderm development [GO:0001701]; positive regulation of cell migration [GO:0042088]; epithelial cell differentiation [GO:0043066]; positive regulation of angiogenesis [GO:0043129]; positive regulation of smooth muscle cell proliferation [GO:0043406]; artery morphogenesis [GO:0045779]; positive chemotaxis [GO:0050918]; cellular response to hypoxia [GO:0071456]; angiogenesis [GO:0001525]; ovarian follicle development [GO:0001541]; patterning of blood vessels [GO:0001569]; response to hypoxia [GO:0001666]; blood vessel remodeling [GO:0001974]; positive regulation of mesenchymal cell proliferation [GO:0002053]; positive regulation of leukocyte migration [GO:0002687]; lactation
VEGFA	
WDR54	
SLC2A14	glucose transport [GO:0015758]; spermatogenesis [GO:0007283]; carbohydrate transport [GO:0008643]; cell differentiation [GO:0030154]; neurological system process [GO:0050877]; multicellular organismal development [GO:0007275]
ANKRD37	
DDIT3	negative regulation of canonical Wnt receptor signaling pathway [GO:0090090]; regulation of transcription, DNA-dependent [GO:0006355]; mRNA transcription from RNA polymerase II promoter [GO:0042789]; positive regulation of transcription, DNA-dependent [GO:0045893]; response to amphetamine [GO:0001975]; negative regulation of CREB transcription factor activity [GO:0032792]; response to hydrogen peroxide [GO:0042542]; positive regulation of apoptosis [GO:0043065]; negative regulation of determination of dorsal identity [GO:2000016]; transcription, DNA-dependent [GO:0006351]; response to DNA damage stimulus [GO:0006974]; ER overload response [GO:0006983]; endoplasmic reticulum unfolded protein response [GO:0030968]; response to endoplasmic reticulum stress [GO:0034976]; negative regulation of sequence-specific DNA binding transcription factor activity [GO:0043433]; regulation of DNA-dependent transcription in response to stress [GO:0043620]; response to oxidative stress [GO:0006979]; cell cycle arrest [GO:0007050]; response to nutrient [GO:0007584]; response to drug [GO:0042493]; cell redox homeostasis [GO:0045454]; embryonic organ development [GO:0048568]; cell cycle [GO:0007049]; aging [GO:0007568]

PFKFB4	fructose 2,6-bisphosphate metabolic process [GO:0006003]; glucose metabolic process [GO:0006006]; glycolysis [GO:0006096]; carbohydrate metabolic process [GO:0005975]
ISG20	DNA catabolic process, exonucleolytic [GO:0000738]; RNA catabolic process [GO:0006401]; negative regulation of apoptosis [GO:0043066]; response to estrogen stimulus [GO:0043627]; type I interferon-mediated signaling pathway [GO:0060337]; cytokine-mediated signaling pathway [GO:0019221]; response to dsRNA [GO:0043331]; regulation of defense response to virus [GO:0050688]; defense response [GO:0006952]; response to virus [GO:0009615]; response to drug [GO:0042493]; defense response to virus [GO:0051607]; cell proliferation [GO:0008283]
VLDLR	memory [GO:0007613]; cellular response to insulin stimulus [GO:0032869]; regulation of canonical Wnt receptor signaling pathway [GO:0060828]; cellular response to interleukin-1 [GO:0071347]; cholesterol metabolic process [GO:0008203]; regulation of bone mineralization [GO:0030500]; cellular response to glucose starvation [GO:0042149]; cellular response to lipopolysaccharide [GO:0071222]; lipid transport [GO:0006869]; receptor-mediated endocytosis [GO:0006898]; nervous system development [GO:0007399]; heart development [GO:0007507]; steroid metabolic process [GO:0008202]; regulation of gene expression [GO:0010468]; lipoprotein metabolic process [GO:0042157]; cellular response to hypoxia [GO:0071456]; response to hypoxia [GO:0001666]; lipid metabolic process [GO:0006629]; endocytosis [GO:0006897]; response to nutrient [GO:0007584]; response to hormone stimulus [GO:0009725]; protein transport [GO:0015031]; cerebral cortex development [GO:0021987]; very-low-density lipoprotein particle clearance [GO:0034447]; response to drug [GO:0042493]; symbiosis, encompassing mutualism through parasitism [GO:0044403]; transport [GO:0006810]; cellular component movement [GO:0006928]; signal transduction [GO:0007165]; cell proliferation [GO:0008283]
MT1X	cellular zinc ion homeostasis [GO:0006882]; cellular metal ion homeostasis [GO:0006875]; response to cadmium ion [GO:0046686]; response to metal ion [GO:0010038]; response to arsenic-containing substance [GO:0046685]; response to toxin [GO:0009636]
GPR160	G-protein coupled receptor protein signaling pathway [GO:0007186]
P4HA1	collagen fibril organization [GO:0030199]; peptidyl-proline hydroxylation to 4-hydroxy-L-proline [GO:0018401]
JMJD1A	histone H3-K9 demethylation [GO:0033169]; chromatin modification [GO:0016568]; positive regulation of transcription, DNA-dependent [GO:0045893]; spermatogenesis [GO:0007283]; androgen receptor signaling pathway [GO:0030521]; formaldehyde biosynthetic process [GO:0046293]; hormone-mediated signaling pathway [GO:0009755]; cell differentiation [GO:0030154]
JMJD2C	histone H3-K9 demethylation [GO:0033169]; chromatin modification [GO:0016568]; regulation of transcription from RNA polymerase II promoter by nuclear hormone receptor [GO:0034339]; regulation of transcription, DNA-dependent [GO:0006355]; positive regulation of cell proliferation [GO:0008284]

KIAA1244	regulation of ARF protein signal transduction [GO:0032012]; exocytosis [GO:0006887]
TNNT1	slow-twitch skeletal muscle fiber contraction [GO:0031444]; regulation of muscle contraction [GO:0006937]; striated muscle contraction [GO:0006941]; muscle filament sliding [GO:0030049]; negative regulation of muscle contraction [GO:0045932]; skeletal muscle contraction [GO:0003009]; protein complex assembly [GO:0006461]; heart development [GO:0007507]; signal transduction [GO:0007165]
BNIP3L	induction of apoptosis [GO:0006917]; mitochondrial protein catabolic process [GO:0035694]; negative regulation of survival gene product expression [GO:0008634]; positive regulation of apoptosis [GO:0043065]; negative regulation of apoptosis [GO:0043066]; defense response to virus [GO:0051607]; negative regulation of cell proliferation [GO:0008285]; interspecies interaction between organisms [GO:0044419]; cellular process [GO:0009987]
CDA	cytidine deamination [GO:0009972]; protein homotetramerization [GO:0051289]; cytosine metabolic process [GO:0019858]; pyrimidine nucleoside salvage [GO:0043097]; negative regulation of nucleotide metabolic process [GO:0045980]; response to cycloheximide [GO:0046898]; pyrimidine base metabolic process [GO:0006206]; pyrimidine-containing compound salvage [GO:0008655]; cellular response to external biotic stimulus [GO:0071217]; cell surface receptor linked signaling pathway [GO:0007166]; negative regulation of cell growth [GO:0030308]; nucleobase, nucleoside and nucleotide metabolic process [GO:0055086]
SAP30	chromatin remodeling [GO:0006338]; negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; histone deacetylation [GO:0016575]; regulation of transcription, DNA-dependent [GO:0006355]; protein import into nucleus, translocation [GO:0000060]; positive regulation of protein binding [GO:0032092]; positive regulation of DNA binding [GO:0043388]
GPI	glucose metabolic process [GO:0006006]; gluconeogenesis [GO:0006094]; negative regulation of caspase activity [GO:0043154]; glucose 6-phosphate metabolic process [GO:0051156]; methylglyoxal biosynthetic process [GO:0019242]; negative regulation of neuron apoptosis [GO:0043524]; glycolysis [GO:0006096]; aldehyde catabolic process [GO:0046185]; angiogenesis [GO:0001525]; carbohydrate metabolic process [GO:0005975]; humoral immune response [GO:0006959]; hemostasis [GO:0007599]; learning or memory [GO:0007611]
GBE1	glycogen biosynthetic process [GO:0005978]; glucose metabolic process [GO:0006006]; glycogen metabolic process [GO:0005977]; carbohydrate metabolic process [GO:0005975]; generation of precursor metabolites and energy [GO:0006091]
WSB1	ubiquitin-dependent protein catabolic process [GO:0006511]; regulation of protein ubiquitination [GO:0031396]; regulation of protein catabolic process [GO:0042176]; regulation of protein stability [GO:0031647]; intracellular signal transduction [GO:0035556]; cellular process [GO:0009987]; biological_process [GO:0008150]

SLC1A1	protein homooligomerization [GO:0051260]; L-glutamate import [GO:0051938]; D-aspartate import [GO:0070779]; dicarboxylic acid transport [GO:0006835]; L-glutamate transport [GO:0015813]; ion transport [GO:0006811]; synaptic transmission [GO:0007268]; transmembrane transport [GO:0055085]
P4HA2	peptidyl-proline hydroxylation to 4-hydroxy-L-proline [GO:0018401]
SLC2A1	glucose transport [GO:0015758]; hexose transport [GO:0008645]; regulation of insulin secretion [GO:0050796]; energy reserve metabolic process [GO:0006112]; water-soluble vitamin metabolic process [GO:0006767]; carbohydrate transport [GO:0008643]; carbohydrate metabolic process [GO:0005975]; vitamin metabolic process [GO:0006766]; response to osmotic stress [GO:0006970]; transmembrane transport [GO:0055085]
ENO2	glucose metabolic process [GO:0006006]; gluconeogenesis [GO:0006094]; response to estradiol stimulus [GO:0032355]; glycolysis [GO:0006096]; response to organic cyclic compound [GO:0014070]; carbohydrate metabolic process [GO:0005975]; response to drug [GO:0042493]
B3GNT4	poly-N-acetyllactosamine biosynthetic process [GO:0030311]; protein glycosylation [GO:0006486]
ANKZF1	

	<p>cytosolic calcium ion concentration [GO:0007204]; activation of JAK2 kinase activity [GO:0042977]; positive regulation of peptidyl-serine phosphorylation of STAT protein [GO:0033141]; positive regulation of Rho protein signal transduction [GO:0035025]; positive regulation of actin filament polymerization [GO:0030838]; positive regulation of interleukin-6 biosynthetic process [GO:0045410]; positive regulation of interleukin-8 biosynthetic process [GO:0045416]; protein homooligomerization [GO:0051260]; response to dexamethasone stimulus [GO:0071548]; activation of MAPK activity [GO:0000187]; anti-apoptosis [GO:0006916]; induction of apoptosis [GO:0006917]; regulation of T cell chemotaxis [GO:0010819]; Rac protein signal transduction [GO:0016601]; actin filament polymerization [GO:0030041]; regulation of estrogen receptor signaling pathway [GO:0033146]; negative regulation of phosphorylation [GO:0042326]; positive regulation of phosphorylation [GO:0042327]; positive regulation of DNA replication [GO:0045740]; negative regulation of G-protein coupled receptor protein signaling pathway [GO:0045744]; positive regulation of oligodendrocyte differentiation [GO:0048714]; activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway [GO:0007205]; JAK-STAT cascade [GO:0007259]; regulation of G-protein coupled receptor protein signaling pathway [GO:0008277]; calcium-mediated signaling [GO:0019722]; cell projection assembly [GO:0030031]; entry into host cell [GO:0030260]; response to prostaglandin E stimulus [GO:0034695]; response to interferon-alpha [GO:0035455]; response to cocaine [GO:0042220]; regulation of apoptosis [GO:0042981]; negative regulation of apoptosis [GO:0043066]; positive regulation of epidermal growth factor receptor activity [GO:0045741]; regulation of calcium-mediated signaling [GO:0050848]; response to prostaglandin D stimulus [GO:0071798]; dendritic cell chemotaxis [GO:0002407]; positive regulation of leukocyte chemotaxis [GO:0002690]; receptor-mediated endocytosis [GO:0006898]; apoptosis [GO:0006915]; induction by virus of host cell-cell fusion [GO:0006948]; inflammatory response [GO:0006954]; G-protein coupled receptor protein signaling pathway [GO:0007186]; integrin-mediated signaling pathway [GO:0007229]; intracellular protein kinase cascade [GO:0007243]; detection of virus [GO:0009597]; positive regulation of cell-cell adhesion [GO:0022409]; regulation of endocytosis [GO:0030100]; regulation of cell migration [GO:0030334]; positive regulation of cell migration [GO:0030335]; negative regulation of cell migration [GO:0030336]; neutrophil chemotaxis [GO:0030593]; positive regulation of interleukin-10 production [GO:0032733]; positive regulation of interleukin-2</p>
ZNF395	<p>regulation of transcription, DNA-dependent [GO:0006355]; response to oxidative stress [GO:0006979]</p>

	elevation of cytosolic calcium ion concentration [GO:0007204]; calcium ion homeostasis [GO:0055074]; cAMP biosynthetic process [GO:0006171]; cAMP-mediated signaling [GO:0019933]; response to glucocorticoid stimulus [GO:0051384]; neural tube closure [GO:0001843]; progesterone biosynthetic process [GO:0006701]; androgen metabolic process [GO:0008209]; response to insulin stimulus [GO:0032868]; odontogenesis of dentine-containing tooth [GO:0042475]; negative regulation of vasoconstriction [GO:0045906]; positive regulation of vasodilation [GO:0045909]; heart development [GO:0007507]; blood circulation [GO:0008015]; positive regulation of heart rate [GO:0010460]; organ regeneration [GO:0031100]; neuron projection regeneration [GO:0031102]; response to lipopolysaccharide [GO:0032496]; positive regulation of anti-apoptosis [GO:0045768]; branching involved in embryonic placenta morphogenesis [GO:0060670]; response to hypoxia [GO:0001666]; regulation of the force of heart contraction [GO:0002026]; response to cold [GO:0009409]; response to wounding [GO:0009611]; response to organic substance [GO:0010033]; response to starvation [GO:0042594]; hormone secretion [GO:0046879]; spongiotrophoblast layer development [GO:0060712]; signal transduction [GO:0007165]; cell-cell signaling [GO:0007267]; female pregnancy [GO:0007565]; aging [GO:0007568]; positive regulation of cell proliferation [GO:0008284]; negative regulation of cell proliferation [GO:0008285]; developmental growth [GO:0048589]
ADM	insulin-like growth factor receptor signaling pathway [GO:0048009]; negative regulation of NF-kappaB transcription factor activity [GO:0032088]; regulation of tumor necrosis factor production [GO:0032680]; positive regulation of cell migration [GO:0030335]; response to lipopolysaccharide [GO:0032496]; positive regulation of cell adhesion [GO:0045785]; signal transduction [GO:0007165]; negative regulation of cell proliferation [GO:0008285]; response to chemical stimulus [GO:0042221]
PDLIM2	glucan biosynthetic process [GO:0009250]; positive regulation of glycogen biosynthetic process [GO:0045725]; glycogen metabolic process [GO:0005977]; DNA replication [GO:0006260]; protein dephosphorylation [GO:0006470]; enzyme linked receptor protein signaling pathway [GO:0007167]; carbohydrate transport [GO:0008643]; carbohydrate metabolic process [GO:0005975]; cell differentiation [GO:0030154]; regulation of cell cycle [GO:0051726]; multicellular organismal development [GO:0007275]; cellular metabolic process [GO:0044237]; primary metabolic process [GO:0044238]; metabolic process [GO:0008152]; regulation of biological process [GO:0050789]
PPP1R3B	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay [GO:0000288]; nuclear-transcribed mRNA poly(A) tail shortening [GO:0000289]; glucose homeostasis [GO:0042593]; RNA metabolic process [GO:0016070]; mRNA metabolic process [GO:0016071]; translation [GO:0006412]; cellular protein metabolic process [GO:0044267]; regulation of translational initiation [GO:0006446]; gene expression [GO:0010467]; translational initiation [GO:0006413]; interspecies interaction between organisms [GO:0044419]
EIF4A2	

PAM	response to estradiol stimulus [GO:0032355]; response to glucocorticoid stimulus [GO:0051384]; protein modification process [GO:0006464]; protein processing [GO:0016485]; response to copper ion [GO:0046688]; central nervous system development [GO:0007417]; heart development [GO:0007507]; limb development [GO:0060173]; response to hypoxia [GO:0001666]; peptide metabolic process [GO:0006518]; response to pH [GO:0009268]; peptide hormone processing [GO:0016486]; response to drug [GO:0042493]; cell communication [GO:0007154]; cellular process [GO:0009987]
ERO1L	chaperone mediated protein folding requiring cofactor [GO:0051085]; protein folding [GO:0006457]; protein modification process [GO:0006464]; protein thiol-disulfide exchange [GO:0006467]; brown fat cell differentiation [GO:0050873]; endoplasmic reticulum unfolded protein response [GO:0030968]; response to temperature stimulus [GO:0009266]; electron transport chain [GO:0022900]; transport [GO:0006810]; oxidation-reduction process [GO:0055114]
PDK3	glucose metabolic process [GO:0006006]; pyruvate metabolic process [GO:0006090]; peptidyl-histidine phosphorylation [GO:0018106]; regulation of acetyl-CoA biosynthetic process from pyruvate [GO:0010510]; protein phosphorylation [GO:0006468]; carbohydrate metabolic process [GO:0005975]; response to drug [GO:0042493]; respiratory gaseous exchange [GO:0007585]
PLOD2	protein modification process [GO:0006464]; response to hypoxia [GO:0001666]

negative regulation of protein autophosphorylation [GO:0031953]; positive regulation of Rho GTPase activity [GO:0032321]; MyD88-dependent toll-like receptor signaling pathway [GO:0002755]; MyD88-independent toll-like receptor signaling pathway [GO:0002756]; toll-like receptor 1 signaling pathway [GO:0034130]; toll-like receptor 2 signaling pathway [GO:0034134]; toll-like receptor 3 signaling pathway [GO:0034138]; toll-like receptor 4 signaling pathway [GO:0034142]; positive regulation of monocyte differentiation [GO:0045657]; positive regulation of transcription from RNA polymerase II promoter [GO:0045944]; microglial cell activation [GO:0001774]; release of cytochrome c from mitochondria [GO:0001836]; toll-like receptor signaling pathway [GO:0002224]; transforming growth factor beta receptor signaling pathway [GO:0007179]; SMAD protein import into nucleus [GO:0007184]; learning [GO:0007612]; positive regulation by host of viral transcription [GO:0043923]; positive regulation of DNA replication [GO:0045740]; negative regulation of transcription, DNA-dependent [GO:0045892]; positive regulation of transcription, DNA-dependent [GO:0045893]; stress-activated MAPK cascade [GO:0051403]; membrane depolarization [GO:0051899]; cellular response to calcium ion [GO:0071277]; axon regeneration [GO:0031103]; leading edge cell differentiation [GO:0035026]; response to hydrogen peroxide [GO:0042542]; negative regulation of DNA binding [GO:0043392]; negative regulation of neuron apoptosis [GO:0043524]; positive regulation of neuron apoptosis [GO:0043525]; cellular response to potassium ion starvation [GO:0051365]; liver development [GO:0001889]; positive regulation of endothelial cell proliferation [GO:0001938]; transcription, DNA-dependent [GO:0006351]; Toll signaling pathway [GO:0008063]; response to organic cyclic compound [GO:0014070]; response to lipopolysaccharide [GO:0032496]; response to cytokine stimulus [GO:0034097]; negative regulation by host of viral transcription [GO:0043922]; positive regulation of smooth muscle cell proliferation [GO:0048661]; response to cAMP [GO:0051591]; SMAD protein signal transduction [GO:0060395]; angiogenesis [GO:0001525]; outflow tract morphogenesis [GO:0003151]; response to radiation [GO:0009314]; response to mechanical stimulus [GO:0009612]; response to drug [GO:0042493]; innate immune response [GO:0045087]; positive regulation of fibroblast proliferation [GO:0048146]; regulation of sequence-specific DNA binding transcription factor activity [GO:0051090]; regulation of cell cycle [GO:0051726]; aging [GO:0007568]; circadian rhythm [GO:0007623]; negative regulation of cell proliferation [GO:0008285]; cellular process [GO:0009987]

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KLF7 negative regulation of transcription from RNA polymerase II promoter [GO:0000122]; regulation of transcription from RNA polymerase II promoter [GO:0006357]; negative regulation of insulin secretion [GO:0046676]; response to morphine [GO:0043278]; positive regulation of transcription, DNA-dependent [GO:0045893]; regulation of cytokine secretion [GO:0050707]; negative regulation of fat cell differentiation [GO:0045599]; transcription, DNA-dependent [GO:0006351]; nervous system development [GO:0007399]; axon guidance [GO:0007411]; dendrite morphogenesis [GO:0048813]; response to drug [GO:0042493]